
*** TX REPORT ***

TRANSMISSION OK

TX/RX NO	1040
CONNECTION TEL	912123183400
SUBADDRESS	
CONNECTION ID	
ST. TIME	09/15 20:26
USAGE T	05 '55
PGS.	9
RESULT	OK

Crystal Mall 1, 7th Floor
1911 South Clark Street
Arlington, VA 22202
Tel.: 703-308-8362
Fax: 703-746-5195

USPTO

Fax

To:	Norman Hanson	From:	Examiner Canella
Fax:	212-318-3400	Pages:	9, inclusive
Phone:		Date:	9/15/03
Re:	09/270,437	CC:	

Urgent **For Review** **Please Comment** **Please Reply** **Please Recycle**

● Comments:

Copies of the attachment to 09/270,437. I apologize for the omission.



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

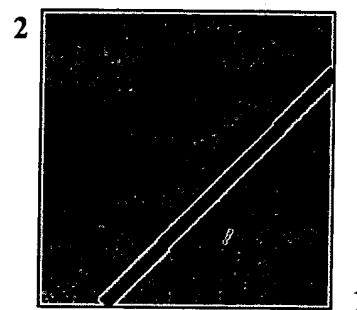
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:5

Matrix **BLOSUM62** ▼ gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 1708 (1 .. 1708)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 854 bits (2206), Expect = 0.0
Identities = 438/445 (98%), Positives = 439/445 (98%)
Frame = +2

Query: 133 RQAIMKLNHGQLENHALKVSYI PDEQITQGPENGRRGGFGSRGQ PRQGSPVAAGAPAKQQ 192
R AIMKLNHGQLENHALKVSYI PDEQI QGPENGRRGGFGSRGQ PRQGSPVAAGAPAKQQ

Sbjct: 32 RGAIMKLNHGQLENHALKVSYI PDEQIAQGPENGRRGGFGSRGQ PRQGSPVAAGAPAKQQ 211

Query: 193 PVDIPLRLLVPTQYVGAI IGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 252
VDIPLRLLVPTQYVGAI IGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG

Sbjct: 212 QVDIPLRLLVPTQYVGAI IGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391

Query: 253 CSSACKMILEIMHKEAKDTKTADEVPLKILAHHNNFVGRLLIGKEGRNLKKVEQDTEKITI 312
CSSACKMILEIMHKEAKDTKTADEVPLKILAHHNNFVGRLLIGKEGRNLKKVEQDTEKITI

Sbjct: 392 CSSACKMILEIMHKEAKDTKTADEVPLKILAHHNNFVGRLLIGKEGRNLKKVEQDTEKITI 571

Query: 313 SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS LQSHLIPGLNLAA 372
SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAA

Sbjct: 572 SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS --SHLIPGLNLAA 745

Query: 373 VGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLS 432
VGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLS

Sbjct: 746 VGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLS 925

Query: 433 RFASASIKIAPPETPDSKVRMV ITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 492
RFASASIKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI

Sbjct: 926 RFASASIKIAPPETPDSKVRMV ITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 1105

Query: 493 RVPASAAGRIGKGGKTVNELQNL TAAEVVVPRDQTPDEN DQVIVKIIGHFYASQMAQRK 552
RVPASAAGRIGKGGKTVNELQNL TAAEVVVPRDQTPDEN DQVIVKIIGHFYASQMAQRK

Sbjct: 1106RVPASAAGRIGKGGKTVNELQNLTAEEVVVPRDQTPDENQVIVKIIIGHFYASQMAQRK 1285

Query: 553 IRDILAQVKQQHQKGQSNLAQARRK 577

IRDILAQVKQQHQKGQSN AQARRK

Sbjct: 1286IRDILAQVKQQHQKGQSNQAQARRK 1360

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 11,732

Number of Sequences: 0

Number of extensions: 7631

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

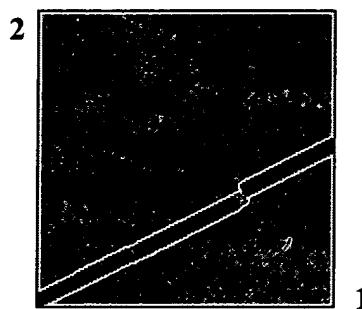
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:6

Matrix **BLOSUM62** ▼ gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 3412 (1 .. 3412)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 775 bits (2000), Expect = 0.0
Identities = 394/603 (65%), Positives = 476/603 (78%), Gaps = 26/603 (4%)
Frame = +1

Query: 1 MNKLYIGNLNESVTPADLEKVFAEHKISYSQFLVKSGYAFVDCPDEHWAMKAIETFSGK 60
MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73 MNKLYIGNLSPAVTADDRLQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIRAIETLSGK 252

Query: 61 VELQGKRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDLSSLAQYGTVENCEQVNTESETA 120
VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253 VELHGKIMEVDYSVSKLRSRKIQIRNIPPHLQWEVLDGLLAQYGTVENVEQVNTESETA 432

Query: 121 VVNVTYSNREQTRQAIMKLNHGQLENHALKVSYI PDEQITQG--PENGRRGGFGSRGQPR 178
VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYI PDE+++ P+ +RG SR Q
Sbjct: 433 VVNVTYATREEAKIAMEKLSGHQFENYSFKISYI PDEEVSSPSPPQRAQRGDHSSREQGH 612

Query: 179 QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQS KIDVHRKENAG 238
A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613 ----APGGTSQARQIDFPLRLILVPTQFVGAIIGKEGLTIKNITKQTQS RVDIHRKENSG 777

Query: 239 AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADEVPLKILAHHNNFVGR LIGKEGRN 298
AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHH VGRLIGKEGRN
Sbjct: 778 AAEKPVTIATPEGTSEACRMILEIMQKEADETKLAEIPLKILAHLNGLVGR LIGKEGRN 957

Query: 299 LKKVEQDTETKITISSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAM 358
LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958 LKKIEHETGKTITISSLQDL SIYNPERTITVKGTVEACASAEIEIMKKLREAFENDMLAV 1137

Query: 359 SLQSHLIPGLNLAAVGLFPASSSAVPPP--PSSVTGAAPYSSFM----- 400
+ Q++LIPGLNL+A+G+F S + PP P AAPY F

Sbjct: 1138NQQANLIPGLNLSALGIFSTGLSVLSPPAGPRGAPPAPYHPFTTHSGYFSSLYPHQFG 1317

Query: 401 -----QAPEQEMVQVFIPAQAVGAIIGKKQHIKQLSRFASASIKIAPPETPDSKVRMV 454

PEQE+V +FIP QAVGAIIGKKG HIKQL+RFA ASIKIAP E PD RMV

Sbjct: 1318PFPHHSYPEQEIVNLFIPTQAVGAIIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMV 1497

Query: 455 VITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHIRVPASAAGRIGKGGKTVNELQ 514

+ITGPPEAQFKAQGRI+GKLKEENFF PKEEVKLE HIRVP+S AGRVIGKGGKTVNELQ

Sbjct: 1498IITGPPEAQFKAQGRIFGKLKEENFPKKEEVKLEAHIRVPSSAGRIVIGKGGKTVNELQ 1677

Query: 515 NLTAEEVVVPRDQTPDENQVIVKIIIGHFYASQMAQRKIRDILAQVKQQHQKGQSNLAQA 574

NLT+AEV+VPRDQTPDEN++VIV+IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A

Sbjct: 1678NLTSAAEVIVVPRDQTPDENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQEQQKYPQGVASQ 1857

Query: 575 RRK 577

R K

Sbjct: 1858RSK 1866

CPU time: 0.07 user secs. 0.00 sys. secs 0.07 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 21,798

Number of Sequences: 0

Number of extensions: 14808

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

c-myc-CRD

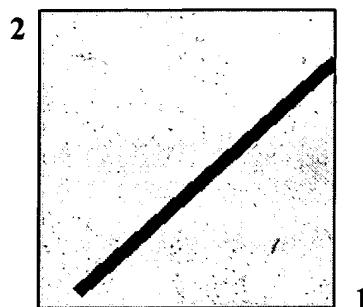
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:7

Matrix **BLOSUM62** ▼ gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 1946 (1 .. 1946)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 963 bits (2489), Expect = 0.0
 Identities = 493/499 (98%), Positives = 494/499 (98%)
 Frame = +3

Query: 79 RSRKIQIRNIPPQLRWEVLDSSLQAQYGTVENCEQVNTESETAVVNVTYSNREQTRQAIMK 138
 RSRKIQIRNIPPQLRWEVLDSSLQAQYGTVENCEQVNTESETAVVNVTYSNREQTRQAIMK
 Sbjct: 108 RSRKIQIRNIPPQLRWEVLDSSLQAQYGTVENCEQVNTESETAVVNVTYSNREQTRQAIMK 287

Query: 139 LNHQLENHALKVSYI PDEQITQGPENGRRGGFGSRGQPRQGSPVAAGAPAKQQPVDIPL 198
 LNHQLENHALKVSYI PDEQI QGPENGRRGGFGSRGQPRQGSPVAAGAPAKQQ VDIPL
 Sbjct: 288 LNHQLENHALKVSYI PDEQIAQGPENGRRGGFGSRGQPRQGSPVAAGAPAKQQQVDIPL 467

Query: 199 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAI SVHSTPEGCSSACK 258
 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAI SVHSTPEGCSSACK
 Sbjct: 468 RLLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAI SVHSTPEGCSSACK 647

Query: 259 MILEIMHKEAKDTKTADEVPLKILAHNNFVGR LIGKEGRNLKKVEQDTETKITISSLQDL 318
 MILEIMHKEAKDTKTADEVPLKILAHNNFVGR LIGKEGRNLKKVEQDTETKITISSLQDL
 Sbjct: 648 MILEIMHKEAKDTKTADEVPLKILAHNNFVGR LIGKEGRNLKKVEQDTETKITISSLQDL 827

Query: 319 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAVGLFPA 378
 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS SHLIPGLNLAAVGLFPA
 Sbjct: 828 TLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAAVGLFPA 1001

Query: 379 SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAPAQAVGAIIGKKQHIKQLSRFASAS 438
 SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAPAQAVGAIIGKKQHIKQLSRFASAS
 Sbjct: 1002 SSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAPAQAVGAIIGKKQHIKQLSRFASAS 1181

Query: 439 IKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHIRVPASA 498
 IKIAPPETPDSKVRMV+ITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHIRVPASA

Sbjct: 1182IKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHIRVPASA 1361

Query: 499 AGRVIGKGGKTVNELQNLAAEVVVPRDQTPDENQVIVKIIIGHFYASQMAQRKIRDILA 558
AGRVIGKGGKTVNELQNLAAEVVVPRDQTPDENQVIVKIIIGHFYASQMAQRKIRDILA

Sbjct: 1362AGRVIGKGGKTVNELQNLAAEVVVPRDQTPDENQVIVKIIIGHFYASQMAQRKIRDILA 1541

Query: 559 QVKQQHQKGQSNLAQARRK 577

QVKQQHQKGQSN AQARRK

Sbjct: 1542QVKQQHQKGQSNQAQARRK 1598

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 13,365

Number of Sequences: 0

Number of extensions: 8706

Number of successful extensions: 15

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 2

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)



Blast 2 Sequences results

PubMed

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OMIM

Taxonomy

Structure

c-myc-CRD

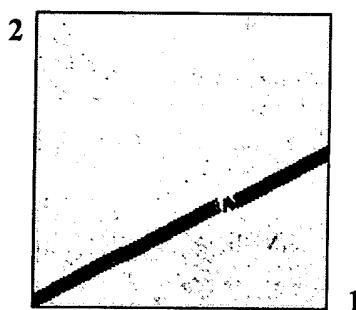
BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.6 [Apr-09-2003]

SEQ ID NO:8

Matrix **BLOSUM62** ▼ gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 577 (1 .. 577)

Sequence 2 lcl|seq_2 Length 3283 (1 .. 3283)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 742 bits (1916), Expect = 0.0
Identities = 381/579 (65%), Positives = 458/579 (78%), Gaps = 2/579 (0%)
Frame = +1

Query: 1 MNKLYIGNLNESVTPADLEKVFAEHKISYSGQFLVKSGYAFVDCPDEHWAMKAIETFSGK 60
MNKLYIGNL+ +VT DL ++F + K+ +GQ L+KSGYAFVD PD++WA++AIET SGK
Sbjct: 73 MNKLYIGNLSPAVTADDLQLFGDRKLPLAGQVLLKSGYAFVDYPDQNWAIRAIETLSGK 252

Query: 61 VELQGKRLEMEHSVPKKQRSRKIQIRNIPPQLRWEVLDSSLQAQYGTVENCEQVNTESETA 120
VEL GK +E+++SV KK RSRKIQIRNIPP L+WEVLD LLAQYGTVEN EQVNT++ETA
Sbjct: 253 VELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLDGLLAQYGTVENVEQVNTESETA 432

Query: 121 VVNVTYSNREQTRQAIMKLNHGQLENHALKVSYIPDEQITQG--PENGRRGGFGSRGQPR 178
VVNVTY+ RE+ + A+ KL+GHQ EN++ K+SYIPDE+++ P+ +RG SR Q
Sbjct: 433 VVNVTYATREEAKIAMEKLSGHQFENYSFKISYIPDEEVSSPSPPQRAQRGDHSSREQGH 612

Query: 179 QGSPVAAGAPAKQQPVDIPLRLLVPTQYVGAIIGKEGATIRNITKQTQS KIDVHRKENAG 238
A G ++ + +D PLR+LVPTQ+VGAIIGKEG TI+NITKQTQS++D+HRKEN+G
Sbjct: 613 ----APGGTSQARQIDFPLRILVPTQFVGAIIGKEGLTIKNITKQTQS RVDIHRKENSG 777

Query: 239 AAEKAISVHSTPEGCSSACKMILEIMHKEAKDTKTADEVPLKILAHHNFVGRLLIGKEGRN 298
AAEK +++H+TPEG S AC+MILEIM KEA +TK A+E+PLKILAHH VGRLLIGKEGRN
Sbjct: 778 AAEKPVTIHATPEGTSEACRMILEIMQKEADETKLAE EIPLKILAHHNGLVGRLLIGKEGRN 957

Query: 299 LKKVEQDTETKITISSLQDLTLYNPERTITVKGAIENCRAEQEIMKKVREAYENDVAAM 358
LKK+E +T TKITISSLQDL++YNPERTITVKG +E C AE EIMKK+REA+END+ A+
Sbjct: 958 LKKIEHETGKTITISSLQDLSIYNPERTITVKGTVEACASAEIEIMKKLREAFENDMLAV 1137

Query: 359 SLQSHLIPGLNLAAVGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVG 418
+ S G F SS P P+ PEQE+V +FIP QAVG

Sbjct: 1138NTHS-----GYF---SSLYPHHQFG----PFPHHHSYPEQEIVNLFIPTQAVG 1260

Query: 419 AIIGKKGQHIKQLSRFASASIKIAPPETPDSKVRMVITGPPEAQFKAQGRIYGKLKEEN 478

AIIGKKG HIKQL+RFA ASIKIAP E PD RMV+ITGPPEAQFKAQGRI+GKLKEEN

Sbjct: 1261AIIGKKGAHKQLARFAGASIKIAPAE GDPVSERMVIITGPPEAQFKAQGRIFGKLKEEN 1440

Query: 479 FFGPKKEEVKLETHIRVPASAAGR VIGKGGKTVNELQNL TAAEVVPRDQTPDEN DQVIVK 538

FF PKEEVKLE HIRVP+SAGR VIGKGGKTVNELQNL T+AEV+VPRDQTPDEN++VIV+

Sbjct: 1441FFNPKEEVKLEAHIRVPSSTAGR VIGKGGKTVNELQNL TSAEVIVPRDQTPDENEEVIVR 1620

Query: 539 IIGHFYASQMAQRKIRDILAQVKQQHQKGQS NLAQARRK 577

IIGHF+ASQ AQRKIR+I+ QVKQQ QK +A R K

Sbjct: 1621IIGHFFASQTAQRKIREIVQQVKQQE QKYPQGVASRSK 1737

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.314	0.131	0.365

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 20,909

Number of Sequences: 0

Number of extensions: 14230

Number of successful extensions: 17

Number of sequences better than 10.0: 2

Number of HSP's better than 10.0 without gapping: 3

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3

length of query: 577

length of database: 2,972,685,411

effective HSP length: 146

effective length of query: 431

effective length of database: 2,972,685,265

effective search space: 1281227349215

effective search space used: 1281227349215

frameshift window, decay const: 50, 0.1

T: 9

A: 40

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 84 (37.0 bits)